prostate tumors. Because HML-2 is a well-recognized family, the skilled person will be able to determine without difficulty whether any particular endogenous retroviruses is or is not a HML-2. Preferred members of the HML-2 family for use in accordance with the present invention are those whose proviral genome has an LTR which has at least 75% sequence identity to SEQ ID NO:150 (the LTR sequence from HML-2.HOM [1]). Example LTRs include SEQ ID NOS:151-154.

Q26 cont.

JB

(23) Delete the paragraph at page 37, lines 20-27 and insert:

Sequences from HERV-K(CH) are shown in SEQ ID NOS:14-39 and have been deposited with the ATCC (see Table 7). The skilled person will be able to classify any further HERV as HERV-K(CH) or not based on sequence identity to these HERV-K(CH) polynucleotides. Preferably such a comparison is to one or more, or all, of the polynucleotide sequences disclosed herein or of the polynucleotide inserts in the ATCC-deposited isolates. Alternatively, the skilled artisan can determine the sequence identity based on a comparison to any one or more, or all, of the sequences in SEQ ID NOS:7-10 and SEQ ID NOS:14-39 taking into consideration the spontaneous mutation rate associated with retroviral replication. Thus, it will be apparent when the differences in the sequences are consistent with a HERV-K(CH) isolate or consistent with another HERV.

Q27

(24) Delete the paragraph at page 38, lines 7-10 and insert:

The invention provides an isolated polynucleotide comprising: (a) the nucleotide sequence of any of SEQ ID NOS:7-10; (b) the nucleotide sequence of any of SEQ ID NOS:27-39; (c) the complement of a nucleotide sequence of any of SEQ ID NOS:7-10; or (d) the complement of the nucleotide sequence of any of SEQ ID NOS:27-39.

Q28

(25) Delete the paragraph at page 38, lines 12-15 and insert:

The invention also provides an isolated polynucleotide comprising a fragment of: (a) a nucleotide sequence shown in SEQ ID NOS:7-10; (b) the nucleotide sequence shown in any of SEQ ID NOS:27-39; (c) the complement of a nucleotide sequence shown in SEQ ID NOS:7-10; or (d) the complement of the nucleotide sequence shown in any of SEQ ID NOS:27-39.

Q29

(26) Delete the paragraph at page 38, lines 22-27 and insert:

The fragment is preferably neither one of the following sequences nor a fragment of one of the following sequences: (i) the nucleotide sequence shown in SEQ ID NO:42; (ii) the

Q30

nucleotide sequence shown in SEQ ID NO:43; (iii) the nucleotide sequence shown in SEQ ID NO:44; (iv) the nucleotide sequence shown in SEQ ID NO:45; (v) a known polynucleotide; or (vi) a polynucleotide known as of 7th December 2000 (*e.g.* a polynucleotide available in a public database such as GenBank of GeneSeq before 7th December 2000).

Q30 cont.

(27) Delete the paragraph at page 39, lines 14-17 and insert:

Preferred fragments (*e.g.* for the identification of HERV-K(CH) polynucleotides associated with cancer) which do not correspond identically in their entirety to any portion of the sequence(s) shown in SEQ ID NOS:42-45 are: SEQ ID NO:59 (from gag region), SEQ ID NOS:60-70 (from pol region) and SEQ ID NOS:71-82 (from 3' pol region).

Q31

JP (28) Delete the paragraph at page 39, lines 17-21 and insert:

Preferred fragments (*e.g.* for the simultaneous identification of HERV-K(CH) polynucleotides, HERV-KII polynucleotides and/or HERV-K10 polynucleotides) which do correspond identically in their entirety to any portion of the sequence(s) shown in SEQ ID NOS:44 & 45 are SEQ ID NOS:83 & 84 (from gag region).

Q32

(29) Delete the paragraph at page 39, line 27, to page 40, line 9 and insert:

The invention also provides an isolated polynucleotide comprising (a) a segment that is a fragment of the sequence shown in SEQ ID NOS:7-10 or SEQ ID NOS:27-39, wherein (i) said fragment is at least 10 nucleotides in length and (ii) corresponds identically in its entirety to a portion of SEQ ID NO:44 and/or 45; and, optionally, (b) one or more segments flanking the segment defined in (a), wherein the presence of said optional segment(s) causes said polynucleotide to not correspond identically to any portion of a sequence shown in SEQ ID NOS:7- 10 or SEQ ID NOS:27-39. In some embodiments, the optional flanking segments share less than 40% sequence identity to the nucleic acid sequences shown in SEQ ID NOS:7-10, SEQ ID NO:44 and/or SEQ ID NO:45. In other embodiments, the optional flanking segments have no contiguous sequence of 10, 12, 15 or 20 nucleotides in common with SEQ ID NOS:7-10, SEQ ID NO:44 and/or SEQ ID NO:45. In yet other embodiments, the optional flanking segment is not present. In further embodiments, a fragment of the polynucleotide sequence is up to at least 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, 1000, or 1500 nucleotides in length.

Q33

(30) Delete the paragraph at page 40, lines 10-19 and insert:

The invention also provides an isolated polynucleotide having formula 5'-A-B-C-3',

Q34

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(b) a HERV-K(CH) sequence as shown in any one of SEQ ID NOS:14-26; (c) a HERV-K(CH) sequence as shown in any one of SEQ ID NOS:27-39; or (d) a fragment of (a), (b) or (c). The fragment of (d) is preferably at least *x* nucleotides in length, wherein *x* is at least 7 (*e.g.* at least 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100 *etc.*).

Q39 Cont

(36) Delete the paragraph at page ~~41~~ 43, lines ~~9-22~~ 9-21 and insert:

Preferred polynucleotides of the invention are those having a sequence set forth in any one of the polynucleotide sequences SEQ ID NOS:7-10 and SEQ ID NOS:14-39 provided herein; polynucleotides obtained from the biological materials described herein, in particular, polynucleotide sequences present in the isolates deposited with the ATCC and having ATCC accession numbers given in Table 7 or other biological sources (particularly human sources) or by hybridization to the above mentioned sequences under stringent conditions (particularly conditions of high stringency); genes corresponding to the provided polynucleotides; variants of the provided polynucleotides and their corresponding genes particularly those variants that retain a biological activity of the encoded gene product (*e.g.* a biological activity ascribed to a gene product corresponding to the provided polynucleotides as a result of the assignment of the gene product to a protein family(ies) and/or identification of a functional domain present in the gene product). Other polynucleotides and polynucleotide compositions contemplated by and within the scope of the present invention will be readily apparent to one of ordinary skill in the art when provided with the disclosure here.

Q40

(37) Delete the paragraph at page 45, lines 9-11 and insert:

The invention provides an isolated polypeptide: (a) encoded within a HERV-K(CH) open reading frame; (b) encoded by a polynucleotide shown in SEQ ID NO:11, 12 or 13; or (c) comprising an amino acid sequence as shown in any one of SEQ ID NOS:46-49, 50-55, 56-57 or 58.

Q41

(38) Delete the paragraph at page 45, lines 12-18 and insert:

~~Deduced polypeptides encoded by the~~ HERV-K(CH) polynucleotides of the invention include the gag translations shown in SEQ IDS 46-49 and the 3' pol translations shown in SEQ ID NOS:50-55. A polypeptide sequence encoded by the polynucleotide having the sequence shown in SEQ ID NO:15 is provided in SEQ ID NO:56; a polypeptide sequence encoded by the

Q42